

sub  
A  
(iii) one or more enzymes that add or remove a moiety to or from said one or more binding partner polypeptides or one or more tagged binding partner polypeptides;

wherein said one or more tagged binding partner polypeptides or said one or more binding partner polypeptides comprise one or more sites for the addition or removal of said moiety, wherein addition or removal of said moiety promotes binding or dissociation of said one or more binding partner polypeptides with the corresponding one or more tagged binding partner polypeptides; under conditions which promote binding or dissociation of said one or more binding partner polypeptides with said one or more tagged binding partners; and

B1  
cont  
B. detecting said binding or dissociation, wherein detection of binding or dissociation as a result of said mixing is indicative of enzyme activity.

B2  
27. (Amended) The method of claim 1 wherein said one or more sites comprise a sequence which directs modification by an enzyme selected from the group consisting of a kinase, a phosphatase, a UDP-N-acetylglucosamine-dolichyl-phosphate-N-acetylglucosamine phosphotransferase, an O-GlcNAc transferase, a glycylpeptide-N-tetradecanoyl transferase, a carbohydrate transferase, a ubiquitin activating enzyme E1, a ubiquitin conjugating enzyme E2, a ubiquitin conjugating enzyme Ubc9, a ubiquitin protein ligase E3, a poly (ADP-ribose) polymerase, a fatty acyl transferase, and an NAD:Arginine ADP ribosyltransferase.

B  
32. The method of claim 1 wherein said tag on said one or more tagged binding partner polypeptides is selected from the group consisting of a coiled-coil, an antigen, an epitope, an antibody, a single chain antibody, a nucleic acid binding domain, a radioactive amino acid, a fluorescent molecule, a reporter enzyme, and biotin.

B  
33. The method of claim 1 wherein said site is recombinant.

B  
34. The method of claim 1 wherein said site is naturally occurring.

B3  
51. A method of screening for a candidate modulator of enzymatic activity comprising:

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C1

A. mixing:

- (i) one or more tagged binding partner polypeptides;
- (ii) one or more binding partner polypeptides that correspond to said one or more tagged binding partner polypeptides of step (i); and
- (iii) one or more enzymes that adds or removes a moiety to or from said binding partner polypeptide or said one or more tagged binding partner polypeptides;

wherein said one or more tagged binding partner polypeptides or said one or more binding partner polypeptides comprise one or more sites for the addition or removal of said moiety, wherein addition or removal of said moiety promotes binding or dissociation of said one or more binding partner polypeptides with the corresponding one or more tagged binding partner polypeptides; under conditions which promote binding or dissociation of said one or more binding partner polypeptides and said one or more tagged binding partner polypeptides; and

B. detecting binding or dissociation of said one or more binding partner polypeptides to said one or more tagged binding partner polypeptides in both the presence and absence of a candidate modulator of enzymatic activity, wherein detection of the amount binding or dissociation in the presence of the candidate modulator that is lesser or greater as compared to the amount of binding or dissociation in the absence of the candidate modulator indicates modulation of enzymatic activity by said candidate modulator.

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#### REMARKS

In response to the Restriction Requirement dated June 18, 2002, Applicants **ELECT** Group I, claims 1-13, 27, 28, 30, 32-34, 51 and 52 for prosecution on the merits, with traverse. Applicants further **ELECT** the species "kinases," with traverse.

Applicants submit, as the basis for their traversal of the Restriction Requirement, that groups I and II are sufficiently related and overlapping to permit a thorough search of each group without undue burden on the Examiner. The restriction between groups I and II is made on the basis of one group being drawn to monitoring enzyme activity by measuring association of a pair of binding partners, while the other monitors dissociation of a pair of binding partners.

Applicants submit that the search will necessarily focus on the measurement of polypeptide